Molecular Ecology 1997, **6**, 1203–1209

Author index

Abbott DH *see* **Faulkes CG**
Abbott RJ *see* **Wolff K**
Abe S *see* **Ishibashi Y**
Akkermans ADL *see* **Sessitsch A**
Akkermans ADL *see* **Wolters DJ**
Alcivar-Warren A *see* **Dhar AK**
Alderson G *see* **Gibbs HL**
All JN *see* **Stewart Jr CN**
Allard MW *see* **Young DL**
Allen PJ *see* **Gemmell NJ**
Alvarez-Buylla E *see* **Quijada A**
Amos W *see* **Reed JZ**
Apostolidis AP, Triantaphyllidis C, Kouvatsi A, Economidis PS. Mitochondrial DNA sequence variation and phylogeography among *Salmo trutta* L. (Greek brown trout) populations, 531
Ardern SL, Lambert DM. Is the black robin in genetic peril? 21
Arduino P *see* **Mosco MC**
Armstrong KF *see* **Nicol D**
Arnold W *see* **Gockel J**
Arntzen JW *see* **Scribner T**
Avise JC *see* **Jones AG**
Avise JC *see* **Ortí G**
Ayres DR, Ryan FJ. The clonal and population structure of a rare endemic plant, *Wyethia reticulata* (Asteraceae): allozyme and RAPD analysis, 761

Bachmann K *see* **Gabrielsen TM**
Bachmann K *see* **Roelofs D**
Bagley MJ, Medrano JF, Gall GAE. Polymorphic molecular markers from anonymous nuclear DNA for genetic analysis of populations, 309
Bakx-Schotman T *see* **van Dijk P**
Balanyà J *see* **Pascual M**
Balloux F *see* **Favre L**
Barbagallo S *see* **Mosco MC**
Barefield K *see* **Strassmann JE**
Barker JHA *see* **Beismann H**
Barry SC *see* **Double MC**
Beacham TD *see* **Miller KM**
Becher SA, Griffiths R. Isolation and characterization of six polymorphic microsatellite loci in the European hedgehog (*Erinaceus europaeus* L.), 89
Beebee TJC *see* **Rowe G**
Beiles A *see* **Owuor ED**
Beismann H, Barker JHA, Karp A, Speck T. AFLP analysis sheds light on distribution of two *Salix* species and their hybrid along a natural gradient, 989
Bellamy AR *see* **Turner SJ**
Bennett H *see* **Walton C**
Bensch S *see* **Westerdahl H**
Bensch S, Price T, Kohn J. Isolation and characterization of microsatellite loci in a *Phylloscopus* warbler, 91
Benzie JAH *see* **Williams ST**
Bernatchez L *see* **Tessier N**
Bernatchez L. Mitochondrial DNA analysis confirms the existence of two glacial races of rainbow smelt *Osmerus mordax* and their reproductive isolation in the St Lawrence River estuary (Québec, Canada), 73
Berrebi P *see* **Chenuil A**
Bérubé M *see* **Palsbøll PJ**
Besansky NJ *see* **Lehmann T**
Bessho Y, Tamura S, Hori H, Tanaka H, Ohama T, Osawa S. Planarian mitochondria sequence heterogeneity: Relationships between the type of cytochrome *c* oxidase subunit I gene sequence, karyotype and genital organ, 129
Beukeboom LW *see* **Ramachandran S**
Bidochka MJ, Walsh SRA, Ramos ME, St. Leger RJ, Carruthers RI, Silver JC, Roberts DW. Cloned DNA probes distinguish endemic and exotic *Entomophaga grylli* fungal pathotype infections in grasshopper life stages, 303
Birt TP *see* **Friesen VL**
Boates JS *see* **Wilson AB**
Bodenes C, Labbe T, Pradere S, Kremer A. General vs. local differentiation between two closely related white oak species, 713
Boesch C *see* **Gagneux P**
Bonetti A *see* **Galeotti P**
Bonhomme F *see* **García de León FJ**
Boursot P *see* **Garza JC**
Bousquet J *see* **Perron M**
Bouvet J *see* **Taberlet P**
Brandl R *see* **Eber S**
Brochmann C *see* **Gabrielsen TM**
Brockman FJ *see* **Chandler DP**
Brown DS *see* **Jones CS**
Brown Gladden JG, Ferguson MM, Clayton JW. Matriarchal genetic population structure of North American beluga whales (*Delphinapterus leucas*, Cetacea: Monodontidae), 1033
Brown JL *see* **Li S-H**
Brown JM, Leebens-Mack JH, Thompson JN, Pellmyr OP, Harrison RG. Phylogeography and host association in a pollinating seed parasite *Greya politella* (Lepidoptera: Prodoxidae), 215
Brownell Jr RL *see* **Rosenbaum HC**
Bruford MW *see* **Faulkes CG**
Brygoo Y *see* **Neuvéglise C**
Bull CM *see* **Cooper SJB**
Bullini L *see* **Mosco MC**
Burke T *see* **Double MC**
Burke T *see* **Rowe G**
Burke T *see* **Scribner T**
Burke T *see* **Taberlet P**
Burt A, Dechairo BM, Koenig GL, Carter DA, White TJ, Taylor JW. Molecular markers reveal differentiation among isolates of *Coccidioides immitis* from California, Arizona and Texas, 781
Butlin RK *see* **Walton C**

Cadd GG *see* **Wasser SK**
Camacho FJ, Gernandt DS, Liston A, Stone JK. Endophytic fungal DNA, the source of contamination in spruce needle DNA, 971
Camarra J-J *see* **Taberlet P**

Cameron CM *see* **Nicol D**
Carranza S *see* **Ramachandran S**
Carruthers RI *see* **Bidochka MJ**
Carter DA *see* **Burt A**
Catzeflis FM *see* **Lavergne A**
Chandler DP, Fredrickson JK, Brockman FJ. Effect of PCR template concentration on the composition and distribution of total community 16S rDNA clone libraries, 475
Chaplin JA, Hebert PDN. *Cyprinotus incongruens* (Ostracoda): an ancient asexual? 155
Chen CA *see* **Smith C**
Chenuil A, Desmarais E, Pouyaud L, Berrebi P. Does polyploidy lead to fewer and shorter microsatellites in *Barbus* (Teleostei: Cyprinidae)? 169
Chikhi L *see* **García de León FJ**
Clapham PJ *see* **Rosenbaum HC**
Clarke MF *see* **Painter J**
Clayton JW *see* **Brown Gladden JG**
Clegg MT *see* **Huttley GA**
Cockburn A *see* **Double MC**
Cockburn A *see* **Double MC**
Cockett NE *see* **Moncrief ND**
Coffin J *see* **Stevens S**
Coffin JW *see* **Wilson GA**
Collins FH *see* **Lehmann T**
Colwell MA *see* **Haig SM**
Congdon BC *see* **Friesen VL**
Congiu L *see* **Galeotti P**
Cook JM *see* **Tay WT**
Cooper SJB, Bull CM, Gardner MG. Characterization of microsatellite loci from the socially monogamous lizard *Tiliqua rugosa* using a PCR-based isolation technique, 793
Cornelius JP *see* **Gillies ACM**
Crawford RL *see* **Ederer MM**
Croset H *see* **Garza JC**
Crozier RH *see* **Luikart G**
Crozier RH *see* **Painter J**
Crozier RH *see* **Tay WT**
Crozier YC *see* **Painter J**

Dallas J *see* **Garza JC**
Dallas JF *see* **Piertney SB**
Dawson D *see* **Double MC**
Dawson IK, Waugh R, Simons AJ, Powell W. Simple sequence repeats provide a direct estimate of pollen-mediated gene dispersal in the tropical tree *Gliricidia sepium*, 179
De Barro PJ *see* **Sunnucks P**
De Vos WM *see* **Sessitsch A**
Debaud J-C *see* **Gryta H**
Dechairo BM *see* **Burt A**
DeLoach DM *see* **Hughes CR**
DeSalle R *see* **Rosenbaum HC**
Desmarais E *see* **Chenuil A**
Deutsch JC *see* **van Oppen MJH**
Dhar AK, Pokras MA, Garcia DK, Evers DC, Gordon ZJ, Alcivar-Warren A. Analysis of genetic diversity in common loon *Gavia immer* using RAPD and mitochondrial RFLP techniques, 581
Dittus WPJ *see* **Keane B**
Dizon AE *see* **O'Corry-Crowe G**
Domingo-Roura X *see* **Shinohara M**
Donegan KK *see* **Widmer F**
Double MC, Cockburn A, Barry SC, Smouse PE. Exclusion probabilties for single-locus paternity analysis when related males compete for matings, 1155
Double MC, Dawson D, Burke T, Cockburn A. Finding the fathers in the least faithful bird: a microsatellite-based genotyping system for the superb fairy-wren *Malurus cyaneus*, 691
Drahos DJ *see* **Staley TE**
Dubois-Paganon C *see* **Taberlet P**
Dueser RD *see* **Moncrief ND**
Dumolin-Lapègue S *see* **Le Corre V**
Dumolin-Lapegue S, Pemonge M-H, Petit RJ. An enlarged set of consensus primers for the study of organelle DNA in plants, 393
Durbin ML *see* **Huttley GA**
Duryadi D *see* **Garza JC**
Dvorak WS *see* **Furman BJ**

Eber S, Brandl R. Genetic differentiation of the tephritid fly *Urophora cardui* in Europe as evidence for its biogeographical history, 651
Economidis PS *see* **Apostolidis AP**
Ederer MM, Crawford RL, Herwig RP, Orser CS. PCP degradation is mediated by closely related strains of the genus *Sphingomonas*, 39
Effosse A *see* **Gryta H**
Egan MG *see* **Rosenbaum HC**
El-Akkad S *see* **Wolff K**
Ellegren H *see* **Merilä J**
Epplen JT *see* **Vrieling K**
Evans BJ, Morales JC, Picker MD, Kelly DB, Melnick DJ. Comparative molecular phylogeography of two *Xenopus* species, *X. gilli* and *X. laevis*, in the southwestern Cape Province, South Africa, 333
Evers DC *see* **Dhar AK**

Fahey TG *see* **Lehmann T**
Fahima T see Owuor ED
Fain SR *see* **Wasser SK**
Faulkes CG, Abbott DH, O'Brien HP, Lau L, Roy MR, Wayne RK, Bruford MW. Micro- and macrogeographical genetic structure of colonies of naked mole rats, *Heterocephalus glaber*, 615
Favre L *see* **Wyttenbach A**
Favre L, Balloux F. Characterization of microsatellite loci in the greater white-toothed shrew *Crocidura russula*, 595
Fenton B *see* **Nicol D**
Ferguson MM *see* **Brown Gladden JG**
Ferris C, King RA, Gray AJ. Molecular evidence for the maternal parentage in the hybrid origin of *Spartina anglica*, 185
Fields RL, Scribner KT. Isolation and characterization of novel waterfowl microsatellite loci: cross-species comparisons and research applications, 199
Fleischer R *see* **Paxinos E**
Frampton C *see* **Nicol D**
Fredrickson JK *see* **Chandler DP**
Friesen VL, Congdon BC, Walsh HE, Birt TP. Intron variation in marbled murrelets detected using analysis of single-stranded conformational polymorphisms, 1047
Frost KJ *see* **O'Corry-Crowe G**
Fuller SJ, Wilson JC, Mather PB. Patterns of differentiation among wild rabbit populations (*Oryctolagus cuniculus* L.) in arid and semi-arid ecosystems of north-eastern Australia, 145

Fumagalli L, Pope LC, Taberlet P, Moritz C. Versatile primers for the amplification of the mitochondrial DNA control region in marsupials, 1199

Furman BJ, Grattapaglia D, Dvorak WS, O'Malley DM. Analysis of genetic relationships of Central American and Mexican pines using RAPD markers that distinguish species, 321

Gabrielsen TM, Bachmann K, Jakobsen KS, Brochmann C. Glacial survival does not matter: RAPD phylogeography of Nordic *Saxifraga oppositifolia*, 831

Gagneux P, Boesch, Woodruff DS. Microsatellite scoring errors associated with noninvasive genotyping based on nuclear DNA amplified from shed hair, 861

Galeotti P, Pilastro A, Tavecchia G, Bonetti A, Congiu L. Genetic similarity in long-eared owl communal winter roosts: a DNA fingerprinting study, 429

Gall GAE *see* Bagley MJ

García de León FJ, Chikhi L, Bonhomme F. Microsatellite polymorphism and population subdivision in natural populations of European sea bass *Dicentrarchus labrax* (Linnaeus, 1758), 51

Garcia DK *see* Dhar AK

Gardner MG *see* Cooper SJB

Garza JC, Dallas J, Duryadi D, Gerasimov S, Croset H, Boursot P. Social structure of the mound-building mouse, *Mus spicilegus*, revealed by genetic analysis with microsatellites, 1009

Gavin TA *see* May B

Gay G *see* Gryta H

Geffen E *see* Moritz C

Geller JB, Walton ED, Grosholz ED, Ruiz GM. Cryptic invasions of the crab *Carcinus* detected by molecular phylogeography, 901

Gemmell NJ, Allen PJ, Goodman SJ, Reed JZ. Interspecific microsatellite markers for the study of pinniped populations, 661

Gerace L *see* Ramachandran S

Gerasimov S *see* Garza JC

Gerlach G *see* Gockel J

Gernandt DS *see* Camacho FJ

Gibbs HL, Miller P, Alderson G, Sealy SG. Genetic analysis of brown-headed cowbirds (*Molothrus ater*) raised by different hosts: data from mtDNA and microsatellite DNA markers, 189

Gibbs HL, Prior KA, Weatherhead PJ, Johnson G. Genetic structure of populations of the threatened eastern massasauga rattlesnake, *Sistrurus c. catenatus*: evidence from microsatellite DNA markers, 1123

Gillies ACM, Cornelius JP, Newton AC, Navarro C, Hernández M, Wilson J. Genetic variation in Costa Rican populations of the tropical timber species *Cedrela odorata* L. assessed using RAPDs, 1133

Gliddon C *see* Rassmann K

Glössl J *see* Steinkellner H

Glover DE *see* Huttley GA

Gockel J, Harr B, Schlötterer C, Arnold W, Gerlach G, Tautz D. Isolation and characterization of microsatellite loci from *Apodemus flavicollis* (rodentia, muridae) and *Clethrionomys glareolus* (rodentia, cricetidae), 597

González-Benito ME *see* Martín C

González-Candelas F *see* Palacios C

Goodman SJ *see* Gemmell NJ

Goodman SJ. R_{ST} Calc: a collection of computer programs for calculating estimates of genetic differentiation from microsatellite data and determining their significance, 881

Gordon ZJ *see* Dhar AK

Graham J, Squire GR, Marshall B, Harrison RE. Spatially dependent genetic diversity within and between colonies of wild raspberry (*Rubus idaeus*) detected using RAPD markers, 1001

Grattapaglia D *see* Furman BJ

Gratto-Trevor CL *see* Haig SM

Gray AJ *see* Ferris C

Griffin S *see* Taberlet P

Griffiths R *see* Becher SA

Grosholz ED *see* Geller JB

Gryta H, Debaud J-C, Effosse A, Gay G, Marmeisse R. Fine scale structure of populations of the ectomycorrhizal fungus *Hebeloma cylindrosporum* in coastal sand dune forest ecosystems, 353

Gullberg A, Olsson M, Tegelström H. Male mating success, reproductive success, and multiple paternity in a natural population of sand lizards: behavioural and molecular genetics data, 105

Haig SM, Gratto-Trevor CL, Mullins TD, Colwell MA. Population identification of western hemisphere shorebirds throughout the annual cycle, 413

Hales D *see* Sunnucks P

Hamilton L *see* McConnell SKJ

Hanotte O *see* Taberlet P

Hansen MM *see* Nielsen EE

Hansen MM, Nielsen EE, Mensberg K-LD. The problem of sampling families rather than populations: relatedness among individuals in samples of juvenile brown trout *Salmo trutta* L., 469

Hansson B *see* Westerdahl H

Hardarson G *see* Sessitsch A

Hare MP *see* Ortí G

Harr B *see* Gockel J

Harrison RE *see* Graham J

Harrison RG *see* Brown JM

Harvey S *see* Taylor EB

Hasselquist D *see* Westerdahl H

Hausser J *see* Wyttenbach A

Hawley WA *see* Lehmann T

Hebert PDN *see* Chaplin JA

Heideman A *see* Moritz C

Hernández M *see* Gillies ACM

Herwig RP *see* Ederer MM

Hewitt GM *see* van Oppen MJH

Hori H *see* Bessho Y

Horsup A *see* Taylor AC

Houston CS *see* Wasser SK

Huang Y-J *see* Li S-H

Hughes CR *see* Strassmann JE

Hughes CR, DeLoach DM. Developing microsatellites when they are rare: trinucleotide repeat loci in the northern mockingbird, *Mimus polyglottos*, 1099

Huttley GA, Durbin ML, Glover DE, Clegg MT. Nucleotide polymorphism in the chalcone synthase-A locus and evolution of the chalcone synthase multigene family of common morning glory *Ipomoea purpurea*, 549

Ihssen PE *see* Stott W

Ims RA *see* Stacy JE

Iriondo JM *see* Martín C

Isagi Y, Suhandono S. PCR primers amplifying microsatellite loci

of *Quercus myrsinifolia* Blume and their conservation between oak species, 897

Ishibashi Y, Saitoh T, Abe S, Yoshida MC. Sex-related spatial kin structure in a spring population of *Clethrionomys rufocanus* as revealed by mitochondrial and microsatellite DNA analyses, 63

Jaarola M *see* Thulin CG
Jakobsen KS *see* Gabrielsen TM
Jakobsen KS *see* Stacy JE
Johnson CN *see* Taylor AC
Johnson G *see* Gibbs HL

Jones AG, Avise JC. Microsatellite analysis of maternity and the mating system in the Gulf pipefish *Syngnathus scovelli*, a species with male pregnancy and sex-role reversal, 203

Jones CS, Noble LR, Lockyer AE, Brown DS, Rollinson D. Species-specific primers discriminate schistosome intermediate hosts: unambiguous PCR diagnosis of *Bulinus forskalii* group taxa (Gastropoda: Planorbidae), 843

Jorde PE *see* Stacy JE
Jørgensen H *see* Palsbøll PJ

Kamau L *see* Lehmann T
Karp A *see* Beismann H

Keane B, Dittus WPJ, Melnick DJ. Paternity assessment in wild groups of toque macaques *Macaca sinica* at Polonnaruwa, Sri Lanka using molecular markers, 267

Keller L *see* Krieger MJB
Kelly DB *see* Evans BJ
King RA *see* Ferris C
Koehler GM *see* Wasser SK
Koenig GL *see* Burt A
Kohn J *see* Bensch S
Korol A *see* Owuor ED
Korves TM *see* May B
Kouvatsi A *see* Apostolidis AP
Kremer A *see* Bodenes C
Kremer A *see* Le Corre V

Krieger MJB, Keller L. Polymorphism at dinucleotide microsatellite loci in fire ant *Solenopsis invicta* populations, 997

Kuperus P *see* Roelofs D

Labbe T *see* Bodenes C
Lambert DM *see* Ardern SL
Larsen AH *see* Palsbøll PJ
Latorre A *see* Pascual M
Lau L *see* Faulkes CG

Lavergne A, Verneau O, Patton JL, Catzeflis FM. Molecular discrimination of two sympatric species of opossum (genus *Didelphis*: Didelphidae) in French Guiana, 889

Lawrence EG *see* Staley TE

Le Corre V, Dumolin-Lapègue S, Kremer A. Genetic variation at allozyme and RAPD loci in sessile oak *Quercus petraea* (Matt.) Liebl.: the role of history and geography, 519

Leebens-Mack J *see* Strand AE
Leebens-Mack JH *see* Brown JM

Lehmann T, Besansky NJ, Hawley WA, Fahey TG, Kamau L, Collins FH. Microgeographic structure of *Anopheles gambiae* in western Kenya based on mtDNA and microsatellite loci, 243

Lenk P, Wink M. A RNA/RNA heteroduplex cleavage analysis to detect rare mutations in populations, 687

Lewis GD *see* Turner SJ
Lexer C *see* Steinkellner H

Li S-H, Huang Y-J, Brown JL. Isolation of tetranucleotide microsatellites from the Mexican jay *Aphelocoma ultramarina*, 499

Lieberman D *see* Schierenbeck KA
Lieberman M *see* Schierenbeck KA

Lieven-Antoniou C, Whittam TS. Specificity in the symbiotic association of *Lotus corniculatus* and *Rhizobium loti* from natural populations, 629

Liston A *see* Camacho FJ
Liston A *see* Quijada A
Lockyer AE *see* Jones CS
Loeschcke V *see* Nielsen EE

Luikart G, Painter J, Crozier RH, Westerman M, Sherwin WB. Characterization of microsatellite loci in the endangered long-footed potoroo *Potorous longipes*, 497

Lushai G *see* Sunnucks P

Maceda L *see* Wirgin I
Maclean N *see* Sunnucks P
Marmeisse R *see* Gryta H
Marshall B *see* Graham J

Martín C, González-Benito ME, Iriondo JM. Genetic diversity within and among populations of a threatened species: *Erodium paularense* Fern. Gonz. & Izco, 813

Mather PB *see* Fuller SJ

May B, Gavin TA, Sherman PW, Korves TM. Characterization of microsatellite loci in the Northern Idaho ground squirrel, *Spermophilus brunneus brunneus*, 399

McConnell SKJ, Ruzzante DE, O'Reilly PT, Hamilton L, Wright JM. Microsatellite loci reveal highly significant genetic differentiation among Atlantic salmon (*Salmo salar* L.) stocks from the east coast of Canada, 1075

McIntosh C *see* Paxinos E
McRae P *see* Moritz C
Medrano JF *see* Bagley MJ
Meelis E *see* Vrieling K
Melnick DJ *see* Evans BJ
Melnick DJ *see* Keane B
Mensberg K-LD *see* Hansen MM

Merilä J, Sheldon BC, Ellegren H. Antagonistic natural selection revealed by molecular sex identification of nestling collared flycatchers, 1167

Michiels NK *see* Ramachandran S
Miller DJ *see* Smith C

Miller KM, Withler RE, Beacham TD. Molecular evolution at *Mhc* genes in two populations of chinook salmon *Oncorhynchus tshawytscha*, 937

Miller P *see* Gibbs HL
Milligan BG *see* Strand AE

Moncrief ND, Cockett NE, Neff AD, Thomas WL, Dueser RD. Polymorphic microsatellites in the meadow vole, *Microtus pennsylvanicus*: conservation of loci across species of rodents, 299

Morales JC *see* Evans BJ
Moritz C see Fumagalli L

Moritz C, Heideman A, Geffen E, McRae P. Genetic population structure of the Greater Bilby, *Macrotis lagotis*, a marsupial in decline, 925

Mosco MC, Arduino P, Bullini L, Barbagallo S. Genetic heterogeneity, reproductive isolation and host preferences in mealy aphids of the *Hyalopterus pruni* complex (Homoptera, Aphidoidea), 667

Mullins TD *see* Haig SM
Mundy N, Winchell CS, Woodruff DS. Genetic differences between the endangered San Clemente Island loggerhead shrike *Lanius ludovicianus mearnsi* and two neighbouring subspecies demonstrated by mtDNA control region and cytochrome *b* sequence variation, 29
Murray RA *see* Wolf PG

Navarro C *see* Gillies ACM
Neff AD *see* Moncrief ND
Neuvéglise C, Brygoo Y, Riba G. 28s rDNA group-I introns: a powerful tool for identifying strains of *Beauveria brongniartii*, 373
Nevo E *see* Owuor ED
Newton AC *see* Gillies ACM
Nicol D, Armstrong KF, Wratten SD, Cameron CM, Frampton C, Fenton B. Genetic variation in an introduced aphid pest (*Metopolophium dirhodun*) in New Zealand and relation to individuals from Europe, 255
Nielsen EE *see* Hansen MM
Nielsen EE, Hansen MM, Loeschcke V. Analysis of microsatellite DNA from old scale samples of Atlantic salmon *Salmo salar*: a comparison of genetic composition over 60 years, 487
Noble LR *see* Jones CS

O'Corry-Crowe G, Suydam RS, Rosenberg A, Frost KJ, Dizon AE. Phylogeography, population structure and dispersal patterns of the beluga whale, *Delphinapterus leucas*, in the western Nearctic revealed by mitochondrial DNA, 955
O'Brien HP *see* Faulkes CG
Ohama T *see* Bessho Y
Olsson M *see* Gullberg A
O'Malley DM *see* Furman BJ
O'Reilly PT *see* McConnell SKJ
Orser CS *see* Ederer MM
Ortí G, Hare MP, Avise JC. Detection and isolation of nuclear haplotypes by PCR–SSCP, 575
Osawa S *see* Bessho Y
Owuor ED, Fahima T, Beiles A, Korol A, Nevo E. Population genetic response to microsite ecological stress in wild barley, *Hordeum spontaneum*, 1177

Pääbo S *see* Petri B
Painter J *see* Luikart G
Painter J, Crozier RH, Crozier YC, Clarke MF. Characterization of microsatellite loci for a co-operatively breeding honeyeater, 1103
Palacios C, González-Candelas F. Analysis of population genetic structure and variability using RAPD markers in the endemic and endangered *Limonium dufourii* (Plumbaginaceae), 1107
Palacios C, González-Candelas F. Lack of genetic variability in the rare and endangered *Limonium cavanillesii* (Plumbaginaceae) using RAPD markers, 671
Palsbøll PJ, Bérubé M, Larsen AH, Jørgensen H. Primers for the amplification of tri- and tetramer microsatellite loci in baleen whales, 893
Parkin DT *see* Wetton JH
Pascual M, Balanyà J, Latorre A, Serra L. Diagnosis of sibling species of *Drosophila* involved in the colonization of North America by *D. subobscura*, 293
Patton JL *see* Lavergne A
Patton JL *see* Ruedi M
Pavlovic N *see* Ramachandran S
Paxinos E, McIntosh C, Ralls K, Fleischer R. A noninvasive method for distinguishing among canid species: amplification and enzyme restriction of DNA from dung, 483
Peacock MM, Smith AT. Nonrandom mating in pikas *Ochotona princeps*: evidence for inbreeding between individuals of intermediate relatedness, 801
Pellmyr OP *see* Brown JM
Pemonge M-H *see* Dumolin-Lapegue S
Perron M, Bousquet J. Natural hybridization between black spruce and red spruce, 725
Peters JM. Microsatellite loci for *Pseudomyrmex pallidus* (Hymenoptera: Formicidae), 887
Petit RJ *see* Dumolin-Lapegue S
Petri B, Pääbo S, von Haeseler A, Tautz D. Paternity assessment and population subdivision in a natural population of the larger mouse-eared bat *Myotis myotis*, 235
Picker MD *see* Evans BJ
Piertney SB, Dallas JF. Isolation and characterization of hypervariable microsatellites in the red grouse *Lagopus lagopus scoticus*, 93
Pilastro A *see* Galeotti P
Pokras MA *see* Dhar AK
Pollard S *see* Taylor EB
Pope LC *see* Fumagalli L
Porteous LA, Seidler RJ, Watrud LS. An improved method for purifying DNA from soil for polymerase chain reaction amplification and molecular ecology applications, 787
Pouyaud L *see* Chenuil A
Powell W *see* Dawson IK
Powell W *see* White G
Pradere S *see* Bodenes C
Price T *see* Bensch S
Prior KA *see* Gibbs HL
Purvis A *see* Stacy JE

Quijada A, Liston A, Robinson W, Alvarez-Buylla E. The ribosomal ITS region as a marker to detect hybridization in pines, 995

Ralls K *see* Paxinos E
Ramachandran S *see* Stewart Jr CN
Ramachandran S, Beukeboom LW, Gerace L, Pavlovic N, Carranza S, Michiels NK. Isolation and characterization of microsatellite loci from the planarian *Dugesia polychroa* (Schmidt) (Platyhelminthes: Tricladida), 389
Ramos ME *see* Bidochka MJ
Rassmann K, Tautz D, Trillmich F, Gliddon C. The microevolution of the Galápagos marine iguana *Amblyrhynchus cristatus* assessed by nuclear and mitochondrial genetic analyses, 437
Raymer PL *see* Stewart Jr CN
Reed JZ *see* Gemmell NJ
Reed JZ, Tollit DJ, Thompson PM, Amos W. Molecular scatology: the use of molecular genetic analysis to assign species, sex and individual identity to seal faeces, 225
Riba G *see* Neuvéglise C
Rico C *see* van Oppen MJH
Roberts DW *see* Bidochka MJ
Robinson TJ *see* van Vuuren BJ
Robinson W *see* Quijada A
Roelofs D, Van Velzen J, Kuperus P, Bachmann K. Molecular

evidence for an extinct parent of the tetraploid species *Microseris acuminata* and *M. campestris* (Asteraceae, Lactuceae), 641
Rollinson D *see* **Jones CS**
Rosenbaum HC, Egan MG, Clapham PJ, Brownell Jr RL, DeSalle R. An effective method for isolating DNA from historical specimens of baleen, 677
Rosenberg A *see* **O'Corry-Crowe G**
Rosendahl S, Taylor JW. Development of multiple genetic markers for studies of genetic variation in arbuscular mycorrhizal fungi using AFLP™, 821
Rowe DJ *see* **Tay WT**
Rowe G, Beebee TJC, Burke T. PCR primers for polymorphic microsatellite loci in the anuran amphibian *Bufo calamita*, 401
Roy MR *see* **Faulkes CG**
Ruedi M, Smith MF, Patton JL. Phylogenetic evidence of mitochondrial DNA introgression among pocket gophers in New Mexico (family Geomyidae), 453
Ruiz GM *see* **Geller JB**
Ruzzante DE *see* **McConnell SKJ**
Ryan FJ *see* **Ayres DR**

Saitoh T *see* **Ishibashi Y**
Saumitou-Laprade P *see* **Vrieling K**
Schierenbeck KA, Skupski M, Lieberman D, Lieberman M. Population structure and genetic diversity in four tropical tree species in Costa Rica, 137
Schlötterer C *see* **Gockel J**
Scribner KT *see* **Fields RL**
Scribner T, Arntzen JW, Burke T. Effective number of breeding adults in *Bufo bufo* estimated from age-specific variation at minisatellite loci, 701
Sealy SG *see* **Gibbs HL**
Seidler RJ *see* **Porteous LA**
Seidler RJ *see* **Widmer F**
Serra L *see* **Pascual M**
Sessitsch A, Hardarson G, Akkermans ADL, De Vos WM. Characterization of *Rhizobium etli* and other *Rhizobium* spp. that nodulate *Phaseolus vulgaris* L. in an Austrian soil, 601
Shaw PW. Polymorphic microsatellite markers in a cephalopod: the veined squid *Loligo forbesi*, 297
Sheldon BC *see* **Merilä J**
Sherman PW *see* **May B**
Sherwin P *see* **Taylor AC**
Sherwin WB *see* **Luikart G**
Shinohara M, Domingo-Roura X, Takenaka O. Microsatellites in the bottlenose dolphin *Tursiops truncatus*, 695
Shorrocks B *see* **Walton C**
Silver JC *see* **Bidochka MJ**
Simons AJ *see* **Dawson IK**
Sipes SD *see* **Wolf PG**
Skupski M *see* **Schierenbeck KA**
Smith AT *see* **Peacock MM**
Smith C, Chen CA, Yang H-P, Miller DJ. A PCR-based method for assaying molecular variation in corals based on RFLP analysis of the ribosomal intergenic spacer region, 683
Smith MF *see* **Ruedi M**
Smouse PE *see* **Double MC**
Snyder M *see* **Wilson AB**
Solís CR *see* **Strassmann JE**
Speck T *see* **Beismann H**
Squire GR *see* **Graham J**
St. Leger RJ *see* **Bidochka MJ**
Stabile J *see* **Wirgin I**
Stacy JE, Jorde PE, Steen H, Ims RA, Purvis A, Jakobsen KS. Lack of concordance between mtDNA gene flow and population density fluctuations in the bank vole, 751
Staley TE, Lawrence EG, Drahos DJ. Variable specificity of Tn7::*lacZY* insertion into the chromosome of root-colonizing *Pseudomonas putida* strains, 85
Steen H *see* **Stacy JE**
Steinkellner H, Lexer C, Turetschek E, Glössl J. Conservation of $(GA)_n$ microsatellite loci between *Quercus* species, 1189
Stevens S, Coffin J, Strobeck C. Microsatellite loci in Columbian ground squirrels *Spermophilus columbianus*, 493
Stewart Jr CN, All JN, Raymer PL, Ramachandran S. Increased fitness of transgenic insecticidal rapeseed under insect selection pressure, 773
Stone JK *see* **Camacho FJ**
Stott W, Ihssen PE, White BN. Inheritance of RAPD molecular markers in late trout *Salvelinus namaycush*, 609
Strand AE, Leebens-Mack J, Milligan BG. Nuclear DNA-based markers for plant evolutionary biology, 113
Strassmann JE, Barefield K, Solís CR, Hughes CR, Queller DC. Trinucleotide microsatellite loci for a social wasp, *Polistes*, 97
Strobeck C *see* **Stevens S**
Strobeck C *see* **Wilson GA**
Suhandono S *see* **Isagi Y**
Sunnucks P *see* **Taylor AC**
Sunnucks P, De Barro PJ, Lushai G, Maclean N, Hales D. Genetic structure of an aphid studied using microsatellites: cyclic parthenogenesis, differentiated lineages, and host specialization, 1059
Suydam RS *see* **O'Corry-Crowe G**

Taberlet P *see* **Fumagalli L**
Taberlet P, Camarra J-J, Griffin S, Uhrès E, Hanotte O, Waits LP, Dubois-Paganon C, Burke T, Bouvet J. Noninvasive genetic tracking of the endangered Pyrenean brown bear population, 869

Takenaka O *see* **Shinohara M**
Tamura S *see* **Bessho Y**
Tanaka H *see* **Bessho Y**
Tautz D *see* **Gockel J**
Tautz D *see* **Petri B**
Tautz D *see* **Rassmann K**
Tavecchia G *see* **Galeotti P**
Tay WT, Cook JM, Rowe DJ, Crozier RH. Migration between nests in the Australian arid-zone ant *Rhytidoponera* sp. 12 revealed by DGGE analyses of mitochondrial DNA, 403
Taylor AC. Titration of heparinase for removal of the PCR-inhibitory effect of heparin in DNA samples, 383
Taylor AC, Horsup A, Johnson CN, Sunnucks P, Sherwin P. Relatedness structure detected by microsatellite analysis and attempted pedigree reconstruction in an endangered marsupial, the northern hairy-nosed wombat, *Lasiorhinus krefftii*, 9
Taylor EB, Harvey S, Pollard S, Volpe J. Postglacial genetic differentiation of reproductive ecotypes of kokanee *Oncorhynchus nerka* in Okanagan Lake, British Columbia, 503
Taylor JW *see* **Burt A**
Taylor JW *see* **Rosendahl S**
Tegelström H *see* **Gullberg A**
Tegelström H *see* **Thulin CG**
Tessier N, Bernatchez L, Wright JM. Population structure and

impact of supportive breeding inferred from mitochondrial and microsatellite DNA analyses in landlocked Atlantic salmon *Salmo salar* L., 735
Thomas WL *see* Moncrief ND
Thompson JN *see* Brown JM
Thompson PM *see* Reed JZ
Thulin CG, Jaarola M, Tegelström H. The occurrence of mountain hare mitochondrial DNA in wild brown hares, 463
Tollit DJ *see* Reed JZ
Triantaphyllidis C *see* Apostolidis AP
Trillmich F *see* Rassmann K
Turetschek E *see* Steinkellner H
Turner GF *see* van Oppen MJH
Turner SJ, Lewis GD, Bellamy AR. A genomic polymorphism located downstream of the *gcvP* gene of *Escherichia coli* that correlates with ecological niche, 1019

Uhrès E *see* Taberlet P

van Dijk P, Bakx-Schotman T. Chloroplast DNA phylogeography and cytotype geography in autopolyploid *Plantago media*, 345
van Oppen MJH, Rico C, Deutsch JC, Turner GF, Hewitt GM. Isolation and characterisation of microsatellite loci in the cichlid fish *Pseudotropheus zebra*, 387
van Vuuren BJ, Robinson TJ. Genetic population structure in the yellow mongoose, *Cynictis penicillata*, 1147
von Haeseler A *see* Petri B
von Schantz T *see* Westerdahl H
Van Dijk C *see* Wolters DJ
Van Velzen J *see* Roelofs D
Verneau O *see* Lavergne A
Volpe J *see* Taylor EB
Vrieling K, Saumitou-Laprade P, Meelis E, Epplen JT. Multilocus DNA fingerprints in the plant *Cynoglossum officinale* L. and their use in the estimation of selfing, 587

Waits LP *see* Taberlet P
Walsh HE *see* Friesen VL
Walsh SRA *see* Bidochka MJ
Walton C, Bennett H, Butlin RK, Shorrocks B. A PCR-based method for detecting rare genotypes in large samples of individuals, 195
Walton ED *see* Geller JB
Wasser SK, Houston CS, Koehler GM, Cadd GG, Fain SR. Techniques for application of fecal DNA methods to field studies of Ursids, 1091
Watrud LS *see* Porteous LA
Waugh R *see* Dawson IK
Wayne RK *see* Faulkes CG
Weatherhead PJ *see* Gibbs HL
Westerdahl H, Bensch S, Hansson B, Hasselquist D, von Schantz T. Sex ratio variation among broods of great reed warblers *Acrocephalus arundinaceus*, 543
Westerman M *see* Luikart G
Wetton JH, Parkin DT. A suite of falcon single-locus minisatellite probes: a powerful alternative to DNA fingerprinting, 119
White BN *see* Stott W
White G, Powell W. Isolation and characterization of microsatellite loci in *Swietenia humilis* (Meliaceae): an endangered tropical hardwood species, 851
White G, Powell W. Cross-species amplification of SSR loci in the Meliaceae family, 1195
White TJ *see* Burt A
Whittam TS *see* Lieven-Antoniou C
Widmer F, Seidler RJ, Donegan KK, Reed GL. Quantification of transgenic plant marker gene persistence in the field, 1
Williams ST, Benzie JAH. Indo-West Pacific patterns of genetic differentiation in the high dispersal starfish *Linckia laevigata*, 559
Wilson AB, Boates JS, Snyder M. Genetic isolation of populations of the gammaridean amphipod, *Corphium volutator*, in the Bay of Fundy, Canada, 917
Wilson GA, Strobeck C, Wu L, Coffin JW. Characterization of microsatellite loci in caribou *Rangifer tarandus*, and their use in other artiodactyls, 697
Wilson J *see* Gillies ACM
Wilson JC *see* Fuller SJ
Winchell CS *see* Mundy N
Wink M *see* Lenk P
Wirgin I, Maceda L, Stabile J. An evaluation of introgression of Atlantic coast striped bass mitochondrial DNA in a Gulf of Mexico population using formalin-preserved museum collections, 907
Withler RE *see* Miller KM
Wolf PG, Murray RA, Sipes SD. Species-independent, geographical structuring of chloroplast DNA haplotypes in a montane herb *Ipomopis* (Polemoniaceae), 283
Wolff K, El-Akkad S, Abbott RJ. Population structure in *Alkanna orientalis* (Boraginaceae) in the Sinai Desert, in relation to its pollinator behaviour, 365
Wolters DJ, Van Dijk C, Zoetendal EG, Akkermans ADL. Phylogenetic characterization of ineffective *Frankia* in *Alnus glutinosa* (L.) Gaertn. nodules from wetland soil inoculants, 971
Woodruff DS *see* Gagneux P
Woodruff DS *see* Mundy N
Wratten SD *see* Nicol D
Wright JM *see* McConnell SKJ
Wright JM *see* Tessier N
Wu L *see* Wilson GA
Wyttenbach A, Favre L, Hausser J. Isolation and characterization of simple sequence repeats in the genome of the common shrew, 797

Yang H-P *see* Smith C
Yoshida MC *see* Ishibashi Y
Young DL, Allard MW. Conservation genetics of the plain pigeon *Columba inornata* in Puerto Rico and the Dominican Republic, 877

Zoetendal EG *see* Wolters DJ

Molecular Ecology 1997, **6**, 1211–1213

Keyword index

16s, 475
16s rDNA, 39, 971
28s rDNA, 373

AFLP, 989
age-specific variation, 701
Alkanna orientalis, 365
allele-specific amplification, 195
allelic dropout, 861
allelic variation, 575
allozyme markers, 667
allozyme(s), 155, 293, 453, 503, 519, 651, 761
Alnus, 971
amplification, 861
analysis of variance, 881
Anatidae, 199
ancient DNA, 677
Anopheles, 243
aphids, 255
apomixis, 671
Arthrobacter, 39
artiodactyls, 697
asexual reproduction, 129
asteroid, 559
ATT repeats, 389
Aureobasidium pullulans, 983
Aves, 877

Bacillus thuringiensis, 773
bacteria, 475
Barbus, 169
bats, 235
Bay of Fundy, 917
Beauveria, 373
beluga whale, 955
bias, 475
biodiversity, 179
biogeography, 283, 559, 651
biological control, 303
biological invasions, 901
biomechanics, 989
biotechnology, 1
bootstrap, 881
Brassica napus, 773
breeding system, 155
brood parasite, 189
brown-headed cowbird, 189
Bufo, 401, 701
Bulinus forskalii, 843

canid, 483
canola, 773
Carcinus aestuarii, 901
Carcinus maenas, 901
Caribbean, 877
caribou, 697
Cedrela, 1133
Cephalopoda, 297
Cetacea, 677
cetacean, 695
Charadriiformes, 413
CHD gene, 1167
chimpanzees, 861
chloroplast DNA (cpDNA), 185, 519, 641
cichilids, 387
Clethrionomys, 751
clonality, 821
clone, 761
cloned DNA probes, 303
coadaptation, 629
coastal sand dunes, 353
coccidioidomycosis, 781
colonization, 293, 345
colony, 429
common shrew, 797
communal roost, 429
comparative phylogeography, 333
competition, 629
concerted evolution, 641
consensus primers, 393
conservation, 235, 531, 735, 851, 1133
conservation genetics, 21, 29, 333, 413, 497, 869, 877, 925, 1123
control region, 145, 559, 677
control region sequence, 615
Corals, 677
Corophium volutator, 917
Costa Rica, 137
cpDNA, 345, 393
Crassostrea, 575
Crodidura russula, 595
cross-species amplification, 697, 1195
crustacean, 155
Cynoglossum officinale, 587
cytochrome *b*, 403, 437, 453, 581
cytochrome-*b* sequence, 615

detection, 373
DGGE, 215, 403
Dicentrarchus labrax, 51
Didelphis, 889
diet, 225
dispersal, 63, 955
D-loop region, 1199
DNA amount regulation, 169
DNA contamination, 983
DNA extraction, 225
DNA fingerprinting, 429, 615, 787, 989
DNA persistence, 1
DNA polymorphisms, 353
DNA pooling, 321
DNA sequencing, 185
Drosophila, 195
Dugesia japonica, 129
Dugesia polychroa, 389

eastern massasauga rattlesnakes, 1123
ecological genetics, 629
ecological risk, 773
ecological variation, 137
ectomycorrhiza, 353
effective population size, 701, 735
Emus orbicularis, 687
endangered plants, 813
endangered species, 333, 483, 671
endemics, 813
enriched library, 851
entomopathogenic fungus, 373
Entomophaga grylli, 303
environmental DNA preparation, 1
environmental stress, 1177
Erodium, 813
ESU, 925
Eubalaena glacialis, 677
European sea bass, 51
exotic fungi, 303
extinct parent, 641

faecal DNA, 225
faeces, 869
Fagaceae, 897, 1189
Falco spp., 119
field experiment, 1
fish, 735
Flavobacterium, 39
fluorescent pseudomonads, 85
F-statistics, 781
fungal endophytes, 983

Galápagos marine iguana, 437
gamergates, 403
Gavia immer, 581
GEM, 85
gender-biased gene flow, 437
gene flow, 651, 735, 751, 773, 877
gene genealogies, 309, 575
genealogies, 113
genetic differentiation, 145, 469, 651, 881
genetic divergence, 667
genetic diversity, 581, 609, 629, 1133
genetic marker(s), 203, 1189
genetic relatedness, 429
genetic typing, 869
genetic variability, 365, 615, 701
genetic variation, 463, 671, 813, 851, 917, 1107
genotyping, 683
glacial survival, 831
Gliricidia, 179
Glomus, 821

GMO, 773
grasshoppers, 303
greater white-toothed shrew, 595
grey-sided vole, 63
ground squirrel, 399, 493
group-I introns, 373
grouse, 93
Gulf of Mexico striped bass, 907

hair, 861, 869
Hebeloma cylindrosporum, 353
Helicoverpa zea, 773
heparin inhibition, 383
heparinase, 383
heteroduplex analysis, 145
heterogeneity, 129
heteroplasmy, 129
heterozygosity, 89, 697
historical population genetics, 677
Hordeum spontaneum, 1177
Hormonema dematioides, 983
host plants, 667
host races, 189
host shifts, 215
host specificity, 629
Hound's-Tongue, 587
Hyalopterus, 667
hybrid inviability, 345
hybrid zones, 283, 453
hybridization, 463, 185, 889, 995
hybrids, 609

inbreeding, 1123
individual identification, 893
Indo-West Pacific, 559
ineffective *Frankia*, 971
intergenic spacer, 683
interlocus gene conversion/recombination, 549
introgression, 463, 907
introgressive hybridization, 725
Ipomopsis aggregata, 283
Ipomopsis tenuituba, 283
ITS, 641, 995

karyotype, 129
kin selection, 97
kin structure, 63
kit fox, 483
kokanee, 503

Lacerta agilis, 105
lactose, 85
Lagomorpha, 463
Lagopus, 93
Lanius, 29
laying date, 543
Lepus, 463
Limonium dufourii, 1107
Limonium, 671
Limulus, 575
linkage, 119
lizard, 793
local extinction, 145
loggerhead shrike, 29
Loligo, 297
long-eared owl *Asio otus*, 429

macropods, 497
male philopatry, 1155
male philopatry, 691
Malurus cyaneus, 691
Mantel test, 519
marsupial(s), 9, 497, 1199
maternal inheritance, 185
maternal lineage, 63
mating behaviour, 801
mating success, 105
mating system, 955
meadow vole, 299
Meliaceae, 851, 1133, 1195
Mendelian inheritance, 609
MetaPhor agarose, 399
Metopoloohium dirhodum, 255
Mexican Jay, 499
MHC, 937
microbial population genetics, 781
microclimate ecology, 1177
microgeographic population structure, 243
microsatellite, 9, 93, 169, 243, 299, 389, 399, 437, 469, 499, 661, 861, 881
microsatellite DNA, 29, 91, 401, 493, 695,
microsatellite DNA markers, 189
microsatellite genotyping, 691, 1155
microsatellites, 199, 225, 235, 267, 387, 487, 497, 51, 595, 597, 697, 793, 797, 851, 869, 887, 897, 925, 97, 997, 1123, 1189, 1195
Microseris, 641
Microtus, 299
migration, 403, 413, 831
minisatellite, 437
minisatellite DNA, 21, 503
minisatellite loci, 701
mitochondrial COI gene, 129
mitochondrial DNA, 29, 73, 463, 469, 503, 531, 677, 901, 925, 955, 1147
molecular ecology, 9, 787
molecular genetics, 105
molecular marker(s), 309, 781, 995
molecular sex identification, 1167
molecular typing, 889
monogamy, 793
Monte Carlo simulation, 1155
Morone saxatilis, 907
morphology, 503, 725
mtDNA, 145, 155, 189, 215, 243, 293, 393, 687, 751, 877, 907
mtDNA polymorphisms, 403
multigene family, 549
multilocus DNA fingerprinting, 801
multilocus DNA fingerprinting $(GATA)_4$, 587
multimale paternity, 615
multiple-tubes approach, 869
museum collections, 907
museum specimens, 677
mutation rates, 119
mycorrhiza, 821

naked mole-rats, 615
natural populations, 195
natural selection, 1167
noninvasive DNA sampling, 483
nonradioactive labelling, 387
nonrandom mating, 801
nrDNA, 995
nuclear haplotypes, 575
nucleotide polymorphism, 549
null alleles, 861

oak, 897
obscura group, 293
octocorals, 683
Oncorhynchus nerka, 503
Oncorhynchus tshawytscha, 937
Osmerus, 73

Pan, 861
parentage, 203, 925
parentage analysis, 119
parthenogenesis, 155
paternal exclusion probability, 691, 1155
paternity, 235, 267, 1155
paternity analysis, 493
PCP degradation, 39
PCR, 51, 93, 113, 195, 199, 383, 387, 389, 393, 475, 787, 843, 861, 897, 1133, 1199
PCR amplifications, 483
PCR conditions, 697
PCR–RAPD, 609
PCR–RFLP, 995
PCR–SSCP, 995
permutation test, 881
PGPR, 85
Phaseolus vulgaris, 601
philopatry, 235, 63
Phylloscopus, 91
phylochondrial DNA, 531
phylogenetic analysis, 39
phylogenetics, 321
phylogeny, 73, 215, 283, 345, 437, 453, 531, 831, 901, 971
phylogeography, 1147
Picea mariana, 725
Picea rubens, 725
Picea, 983
pikas, 801
pines, 995
pinnipeds, 225, 661
Pinus, 321
pioneer species, 353
planarian, 389
plant organelle, 393
plant–insect interactions, 215

platyhelminth, 389
Pleistocene, 345
Plutella xylostella, 773
point mutations, 687
pollen-mediated gene dispersal, 179
pollination, 365
polyandry, 203
polygyny, 403, 543
polymorphism, 51, 751, 937
polyploids, 641
polyploidy, 345
ponerine ant, 403
population, 813, 937
population biology, 761
population bottlenecks, 21
population cycles, 751
population differentiation, 413, 519, 781
population genetic structure, 1123
population genetics, 199, 243, 297, 309, 453, 559, 661, 687, 735, 893, 997, 1177
population replacement, 773
population sampling, 469
population structure, 29, 137, , 353, 365, 531, 917, 955, 997
population subdivision, 51, 549
postglacial dispersal, 73
postglacial expansion, 651
primer(s), 91, 93, 113, 299, 399, 1199
probability of paternal exclusion, 493
propagation, 989
Pseudomonas, 39
Pseudomyrmex pallidus, 887
Pseudotropeus, 387

quantitative PCR, 1
Quercus, 897, 1189
Quercus petraea, 519, 713
Quercus robur, 713

rabies, 1147
RAPD, 321, 413, 519, 543, 581, 641, 725, 761, 813, 1177
RAPD–PCR, 255, 917
RAPDs, 137, 293, 365, 671, 831, 843, 1133
rapidly evolving, 549
rare genotypes, 195
rare plants, 761
recolonization, 9, 97, 63, 145, 821, 469, 887
RE–PCR, 781
repeat motif, 169
reproductive ecotypes, 503
reproductive output, 267
reproductive success, 105
restriction sites, 215
RFLP, 559, 581
rhizobial diversity, 601
Rhizobium etli, 601
Rhizobium–legume symbiosis, 629
Rhizospaera kalkhoffii, 983
Rhytidoponera sp. 12 (cf. *mayri*), 403
risk assessment, 1
RNA–RNA heteroduplex, 687
Rodentia, 453
rodents, 597
rRNA, 475
R_{ST}, 881

Salix, 989
Salmo salar, 487
Salmo trutta, 469, 531
salmonid(s), 609, 937
Salvelinus namaycush, 609
Saxifraga oppositifolia, 831
scales, 487
Sciuridae, 493
scleractinians, 683
scnDNA, 309
sediment, 475
seed dispersal, 365
sequence, 937
sex differences, 1167
sex ratios, 543
sexual dimorphism, 203, 1167
sexual selection, 203, 543
shorebirds, 413
sibling species, 293, 667, 889, 901
simple sequence repeats, 179, 1189
simple sequences, 89
simultaneous hermaphrodite, 389
single-copy DNA, 113
single-locus DNA marker(s), 387, 897
single-locus profiling, 119
skink, 793
slippage-deletion bias, 169
slipped-strand mispairing, 169
smelt, 73
social structure, 403
sociality, 97
soil, 85
soil DNA, 787
soil DNA purification, 787
Solenopsis invicta, 997
song repertoire size, 543
Soricidae, 595, 797
South Africa, 333
speciation, 667, 283
species differentiation, 713
species-specific DNA markers, 725
species-specific primers, 843
Spermophilus columbianus, 493
Spermophilus, 399
Sphingomonas, 39
squid, 297
SSCP, 309, 575, 713
SSRs, 797
stocking, 735
Stoffel fragment, 255
subspecies, 877
substitution rate heterogeity, 549
suction trap, 255
superb fairy-wren, 691
survival, 1167
Swietenia humilis, 851
Sylvidae, 91
synthetic oligonucleotide probes, 587

taxonomy, 321
temperature gradient gel eletrophoresis, 145
temporal and spatial variation, 255
temporal variation, 487
tetranucleotide, 793
Tiliqua rugosa, 793
toad, 401
toque macaques, 267
transposon, 85
trincleotide, 887
trinucleotide repeats, 97
$tRNA^{Leu1}$ intron, 185
tropical forestry, 321
tropical freshwater snails, 843
tropical trees, 137
Tursiops truncatus, 695

Urophora cardui, 651
Ursus arctos, 869

Vespidae, 97
VNTR, 119, 225, 893
voles, 751

waterfowl, 199
whales, 893
wild barley, 1177
wombat, 9

Xenopus gilli, 333
Xenopus laevis, 333

yellow mongoose, 1147